



## SEQUENCE LISTING

<110> Zavada, Jan  
Pastorekova, Silvia  
Pastorek, Jaromir

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<141> 2001-09-27

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gaggatctac ctggagagga ggatctacct gaagttaagc ctaaatacaga agaagagggc 360
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 <222> (1)..(131)  
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gaataataaa	taaaagaagt	ggcatgtcag	gacctcacct	gaaaagccaa	acacagaatc	960
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 <222> (1)..(1334)  
 <223> 6th MN intron

<400> 44								
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aaaacaagac	caaaaaatgg	tgtttgga	ttgtcaaggt	caagtctgga	gagctaaact			600
ttttctgaga	actgtttatc	tttaataagc	atcaaata	ttactttgt	aaatactttt			660
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agacctttta	ggtttctgct	agactaggt	gaactctgcc	tttgcatctc	ttgtgtctgt			780
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gatcctcttc	acag							1334

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 <222> (1)..(512)  
 <223> 7th MN intron

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 cacgttgagg ggctgaggtg ggagaatggg ttgagcccag gagttcaaga caaggcgggg 180  
 caacatagtg tgaccccatc tctacaaaaa aaaccccaac aaaaccaaaa atagccgggc 240  
 atgggtggtat gcggcctagt cccagctact caaggaggct gaggtgggaa gatcgcttga 300  
 ttccaggagt ttgagactgc agtgagctat gatcccacca ctgcctacca tcttttaggat 360  
 acatttatatt atttataaaa gaaatcaaga ggctggatgg ggaatacagg agctggaggg 420  
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 aaccaccca cactgtccac tgacctccct ag 512

<210> 46  
 <211> 114  
 <212> DNA  
 <213> HUMAN

<220>  
 <221> intron  
 <222> (1)..(114)  
 <223> 8th MN intron

<400> 46  
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 gtgtctgtca ttgggtgtca cagccgcct ctcacatctc ctttttctct ccag 114

<210> 47  
 <211> 617  
 <212> DNA  
 <213> HUMAN

<220>  
 <221> intron  
 <222> (1)..(617)  
 <223> 9th MN intron

<400> 47  
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 atattagaga ggcagatcat ggtggggatt ccccatgtgt ccccagaggc taattgatta 180  
 gaatgaagct tgagaaatct cccagcatcc ctctcgcaaa agaatcccc cccctttttt 240  
 taaagatagg gtctcactct gtttgcccca ggctgggggt ttgtggcacg atcatagctc 300  
 actgcagcct cgaactccta ggctcaggca atcctttcac cttagcttct caaagcactg 360  
 ggactgtagg catgagccac tgtgcctggc cccaaacggc ccttttactt ggcttttagg 420  
 aagcaaaaac ggtgcttatc ttacctcttc tcgtgtatcc accctcatcc cttggctggc 480

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 <211> 130  
 <212> DNA  
 <213> HUMAN

<220>  
 <221> intron  
 <222> (1)..(130)  
 <223> 10th MN intron

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 gtacacacag 130

<210> 49  
 <211> 1401  
 <212> DNA  
 <213> HUMAN

<400> 49  
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 tacaggcatg cgccaccacg cccggctaatt ttttgtattt ttagtagaga cggggtttcg 180  
 ccatgtttgg tgggctgggc tcgaactcct gatctcaggt gatccaacca ccctggcctc 240  
 ccaaagtgcg gggattatag gcgtgagcca cagcgcctgg cctgaagcag ccactcactt 300  
 ttacagaccc taagacaatg attgcaagct ggtaggattg ctgtttggcc caccagctg 360  
 cgggtgttgc tttgggtgcg gtctcctgtg ctttgcacct ggcccgctta aggcatttgt 420  
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 gattggggct ctaagcttga gcgggttcac cttttcattt atacagggga tgaccagagt 540  
 cattggcgct atggaggtga gacaccacc cgctgcacag acccaatctg ggaaccacgc 600  
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 caccgtccca cccctcacc ttttctaccc gggttcccta agttcctgac ctaggcgtca 720  
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 gcgcaacaat ggccacagtg gtgagggggg ctccccgcgc agacttgggg atggggcggg 960  
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 <211> 59  
 <212> PRT  
 <213> HUMAN

<400> 50

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Glu Asp Ser Pro Arg Glu Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro  
20 25 30

Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Glu Val Lys Pro  
35 40 45

Lys Ser Glu Glu Glu Gly Ser Leu Lys Leu Glu  
50 55

<210> 51

<211> 257

<212> PRT

<213> HUMAN

<400> 51

Gly Asp Asp Gln Ser His Trp Arg Tyr Gly Gly Asp Pro Pro Trp Pro  
1 5 10 15

Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp Ile  
20 25 30

Arg Pro Gln Leu Ala Ala Phe Cys Pro Ala Leu Arg Pro Leu Glu Leu  
35 40 45

Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn Asn  
50 55 60

Gly His Ser Val Gln Leu Thr Leu Pro Pro Gly Leu Glu Met Ala Leu  
65 70 75 80

Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp Gly  
85 90 95

Ala Ala Gly Arg Pro Gly Ser Glu His Thr Val Glu Gly His Arg Phe  
100 105 110

Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg Val  
115 120 125

Asp Glu Ala Leu Gly Arg Pro Gly Gly Leu Ala Val Leu Ala Ala Phe  
130 135 140

Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Gln Leu Leu Ser  
145 150 155 160

Arg Leu Glu Glu Ile Ala Glu Glu Gly Ser Glu Thr Gln Val Pro Gly  
165 170 175

Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe Ser Arg Tyr Phe Gln  
180 185 190

Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala Gln Gly Val Ile Trp  
 195 200 205

Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala Lys Gln Leu His Thr  
 210 215 220

Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu Asn  
 225 230 235 240

Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser Phe  
 245 250 255

Pro

<210> 52  
 <211> 20  
 <212> PRT  
 <213> HUMAN

<400> 52  
 Ile Leu Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala  
 1 5 10 15

Phe Leu Val Gln  
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<210> 53  
 <211> 25  
 <212> PRT  
 <213> HUMAN

<400> 53  
 Met Arg Arg Gln His Arg Arg Gly Thr Lys Gly Gly Val Ser Tyr Arg  
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Pro Ala Glu Val Ala Glu Thr Gly Ala  
 20 25

<210> 54  
 <211> 59  
 <212> PRT  
 <213> HUMAN

<400> 54  
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 1 5 10 15

Glu Pro Ser Pro Ser Glu Glu Pro Phe Pro Ser Val Arg Pro Phe Pro  
 20 25 30

Ser Val Val Leu Phe Pro Ser Glu Glu Pro Phe Pro Ser Lys Glu Pro  
 35 40 45

Ser Pro Ser Glu Glu Pro Ser Ala Ser Glu Glu  
50 55

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<212> RNA  
<213> HUMAN

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cugcaaaaagg gcgcucugug agucagccug cuccccucca ggcuuugcucc uccccacccc 180  
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uccaggccuc acugugcaac ugcugcuguc acugcugcuu cuggugccug uccaucacca 360  
gagguugccc cggaugcagg aggauucccc cuugggagga ggcucuucug gggaagauga 420  
cccacugggc gaggaggauu ugcccaguga agaggauuca cccagagagg 470

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<211> 292  
<212> DNA  
<213> HUMAN

<400> 56  
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agtagctggg actacaggcg cccgccacca tgcccggcta attttttcta tttttggtag 180  
agacgggggt tcaccgtgtt agccagaatg gtctcgatct cctgacttcg tgatccacc 240  
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<210> 57  
<211> 262  
<212> DNA  
<213> HUMAN

<400> 57  
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tagctgggac tacaggcaca tgccattaca cctggcta at tttttgtat ttctagtaga 180  
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cacctcagcc tcccaaatg ag 262

<210> 58  
<211> 2501  
<212> DNA  
<213> HUMAN

<220>  
<221> misc\_feature  
<222> (1)..(2501)  
<223> region 5' to transcription initiation site as determined by RNase protection assay (nucleotide 3507 of Figures 2A-2F and of SEQ ID NO: 5),



corresponding to region of SEQ ID NO: 5 and Figures 2A-2F from nucleotide (7) to nucleotide (2507), in which region some regulatory elements are probably situated.

<220>

<221> unsure what base is at position 1968

<222> (1968)

<223> unsure of base at position 1968, which is the same unknown base as that at position 1974 of SEQ ID NO. 5, i.e., the full-length MN genomic sequence, and of that unknown at position 1968 of SEQ ID NO: 90, and unknown at position 647 of SEQ ID NO: 110. That unknown base is in the 5' region flanking the transcription initiation site (3507) as determined by RNase protection assay.

<400> 58

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gcatgctcgt taagagtcac caccaatccc taatctcaag taatcaggga cacaaacact 180
gcggaaggcc gcagggtcct ctgcctagga aaaccagaga cctttgttca cttgtttatc 240
tgaccttccc tccactattg tccatgaccc tgccaaatcc ccctctgtga gaaacaccca 300
agaattatca ataaaaaaat aaatttaaaa aaaaaatata aaaaaaaaaa aaaaaaaaaa 360
aaaagactta cgaatagtta ttgataaatg aatagctatt ggtaaagcca agtaaagtat 420
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cattgtcatt ctttggattc actagattag tcatcatcct caaaattctc cccaagtctc 540
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aagataattt gtctttaaca gaatcaataa tataatccct taaaggatta tatctttgct 2160
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<210> 59  
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 <213> HUMAN

<220>  
 <221> misc\_feature  
 <222> (1)

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 gacggggttt caccgtgtta gccagaatgg tctcgatctc ctgacttcgt gatccaccgc 240  
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<210> 60  
 <211> 262  
 <212> DNA  
 <213> HUMAN

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 acctcagcct cccaaaatga gg 262

<210> 61  
 <211> 294  
 <212> DNA  
 <213> HUMAN

<400> 61  
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 agacgggggt tcgccatgtt ggtcaggctg gtctcgaaact cctgatctca ggtgatccaa 240  
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 <212> DNA  
 <213> HUMAN

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<210> 63  
 <211> 289  
 <212> DNA  
 <213> HUMAN

<400> 63  
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 aaatacgaaa aaatagccag gcgtgggtggc gggcgcctgt aatcccagct actcgggagg 180  
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 <212> DNA  
 <213> HUMAN

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<400> 65  
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<210> 66  
 <211> 83  
 <212> DNA  
 <213> HUMAN

<400> 66  
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 aggcatgagc cactgtgcct ggc 83

<210> 67  
 <211> 11  
 <212> DNA  
 <213> HUMAN

<400> 67  
 agaaggtaag t 11

<210> 68	
<211> 11	
<212> DNA	
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tggaggtgag a	11
<210> 69	
<211> 11	
<212> DNA	
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<400> 69	
cagtcgtgag g	11
<210> 70	
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ccgaggtgag c	11
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tggaggtacc a	11
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ggaaggtcag t	11
<210> 73	
<211> 11	
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<400> 73	
agcaggtggg c	11
<210> 74	

<211> 11  
<212> DNA  
<213> HUMAN

<400> 74  
gccaggtaca g 11

<210> 75  
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<212> DNA  
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<400> 75  
tgctggtgag t 11

<210> 76  
<211> 11  
<212> DNA  
<213> HUMAN

<400> 76  
cacaggtatt a 11

<210> 77  
<211> 11  
<212> DNA  
<213> HUMAN

<400> 77  
atacagggga t 11

<210> 78  
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<400> 78  
ccccaggcga c 11

<210> 79  
<211> 11  
<212> DNA  
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<400> 79  
acgcagtgca a 11

<210> 80  
<211> 11  
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<210> 81 <211> 11 <212> DNA <213> HUMAN	
<400> 81 ccccaggagg g	11
<210> 82 <211> 11 <212> DNA <213> HUMAN	
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<400> 84 ctccagtcca g	11
<210> 85 <211> 12 <212> DNA <213> HUMAN	
<400> 85 tcgcaggtga ca	12
<210> 86 <211> 11 <212> DNA <213> HUMAN	
<400> 86 acacagaagg g	11

<400> 87

Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp Leu Pro Ser Glu Glu  
20 25 30

Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Glu Val Lys Pro Lys  
50 55 60

Ala Pro Gly Asp Pro Gln Glu Pro Gln Asn Asn Ala His Arg Asp Lys  
85 90 95

Pro Arg Val Ser Pro Ala Cys Ala Gly Arg Phe Gln Ser Pro Val Asp  
115 120 125

Leu Leu Gly Phe Gln Leu Pro Pro Leu Pro Glu Leu Arg Leu Arg Asn  
145 150 155 160

Leu Gly Pro Gly Arg Glu Tyr Arg Ala Leu Gln Leu His Leu His Trp  
180 185 190

Phe Pro Ala Glu Ile His Val Val His Leu Ser Thr Ala Phe Ala Arg  
210 215 220

Phe Leu Glu Glu Gly Pro Glu Glu Asn Ser Ala Tyr Glu Gln Leu Leu  
245 250 255

31

260	265	270
Gly Leu Asp Ile Ser Ala Leu Leu Pro Ser Asp Phe Ser Arg Tyr Phe		
275	280	285
Gln Tyr Glu Gly Ser Leu Thr Thr Pro Pro Cys Ala Gln Gly Val Ile		
290	295	300
Trp Thr Val Phe Asn Gln Thr Val Met Leu Ser Ala Lys Gln Leu His		
305	310	315
Thr Leu Ser Asp Thr Leu Trp Gly Pro Gly Asp Ser Arg Leu Gln Leu		
	325	330
Asn Phe Arg Ala Thr Gln Pro Leu Asn Gly Arg Val Ile Glu Ala Ser		
	340	345
Phe Pro Ala Gly Val Asp Ser Ser Pro Arg Ala Ala Glu Pro Val Gln		
	355	360
Leu Asn Ser Cys Leu Ala Ala Gly Asp		
370	375	

<210> 88  
 <211> 34  
 <212> DNA  
 <213> HUMAN

<400> 88  
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<210> 89  
 <211> 34  
 <212> DNA  
 <213> HUMAN

<400> 89  
 attcctctag acagttaccg gctccccctc agat 34

<210> 90  
 <211> 3532  
 <212> DNA  
 <213> HUMAN

<220>  
 <221> misc\_feature which includes the MN gene promoter  
 <222> (1)..(3532)  
 <223> region including the transcription initiation site (nucleotide 3507 of SEQ ID NO: 5 and of Figures 2A-2F) as determined by RNase protection assay, which region is inclusive of the MN gene promoter, and corresponds to nucleotide 7 to nucleotide 3538 of SEQ ID NO: 5 and of Figures 2A-2F.

<220>  
 <221> unsure what base is at position 1968



<222> (1968)

<223> unsure of the base at position 1968, which is the same unknown base at position 1974 of SEQ ID NO: 5 (the full-length MN genomic sequence), position 1968 of SEQ ID NO: 58 and position 647 of SEQ ID NO: 110. That unknown base is in the region that includes the transcription initiation site (nucleotide 3507 of SEQ ID NO: 5 and of Figures 2A-2F) as determined by RNase protection assay, which region is inclusive of the MN gene promoter.

<400> 90

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tgttgactcg tgaccttacc cccaaccctg tgctctctga aacatgagct gtgtccactc 60
aggggttaaat ggattaaggc cgggtgcaaga tgtgctttgt taaacagatg cttgaaggca 120
gcatgctcgt taagagtcac caccaatccc taatctcaag taatcaggga cacaaacact 180
gcggaaggcc gcagggtcct ctgcctagga aaaccagaga cctttgttca cttgtttatc 240
tgaccttccc tccactattg tccatgaccc tgccaaatcc ccctctgtga gaaacaccca 300
agaattatca ataaaaaaaaa aaatttaaaa aaaaaataca aaaaaaaaaa aaaaaaaaaa 360
aaaagactta cgaatagtta ttgataaatg aatagctatt ggtaaagcca agtaaagtat 420
catattcaaa accagacggc catcatcaca gctcaagtct acctgatttg atctctttat 480
cattgtcatt ctttgattc actagattag tcatcatcct caaaattctc cccaagtctc 540
taattacgtt ccaaacattt aggggttaca tgaagcttga acctactacc ttctttgctt 600
ttgagccatg agttgtagga atgatgagtt tacaccttac atgctgggga ttaatttaaa 660
ctttacctct aagtcagttg ggtagccttt ggcttatttt tgtagctaata tttgtagtta 720
atggatgcac tgtgaatcct gctatgatag ttttcctcca cactttgcca ctaggggtag 780
gtaggctactc agttttcagt aattgcttac ctaagaccct aagccctatt tctcttgtag 840
tggcctttat ctgtaatatg ggcatattta atacaatata atttttgagg tttttttgtt 900
tgtttgtttg tttgtttttt tgagacggag tcttgcatct gtcatgcccga ggctggagta 960
gcagtgggtgc catctcggct cactgcaagc tccacctccc gagttcacgc cattttcctg 1020
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gtatttttgg tagagacggg gtttcaccgt gttagccaga atggctctga tctcctgact 1140
tcgtgatcca cccgcctcgg cctcccaaaag ttctgggatt acaggtgtga gccaccgcac 1200
ctggccaatt ttttgagtct ttaaaagtaa aaatatgtct tgtaagctgg taactatggt 1260
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tgcacaaagt gagaacatat aatgtctgca tgtttccata tttcaggaat gtttgcttgt 1740
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tttcttctct actgtgttaa aaaaaagtat gatcttgctc tgagagggtga ggcattctta 2040
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aagataattt gtctttaaca gaatcaataa tataatccct taaaggatta tatctttgct 2160
gggcgcagtg gctcacacct gtaatcccag cactttgggt ggccaagggt gaaggatcaa 2220
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gatattgaca ggggttgccc tcaactacta gattgtgagc tctgtctcag ggcaggtagc 2340
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atttttttgt atttctagta gagacagggt ttggccatgt tgcccgggct ggtctcgaac 2580
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tgttgaatgc aatagtaaat agcatttctc ggagcaagaa ctagattaac aaagggtggt 2760
aaagggttgg agaaaaaaat aatagtttaa tttggctaga gtatgaggga gagtagtagg 2820
agacaagatg gaaaggctctc ttgggcaagg ttttgaagga agttggaagt cagaagtaca 2880
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caatgtgcat	atcgtggcag	gcagtgggga	gccaatgaag	gctttttgagc	aggagagtaa	2940
tgtgttgaaa	aataaatata	ggttaaaccct	atcagagccc	ctctgacaca	tacacttgct	3000
tttcattcaa	gctcaagttt	gtctcccaca	taccattac	ttaaactcacc	ctcgggctcc	3060
cctagcagcc	tgccctacct	ctttacctgc	ttcctggtgg	agtcagggat	gtatacatga	3120
gctgctttcc	ctctcagcca	gaggacatgg	ggggccccag	ctccccctgcc	tttcccccttc	3180
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aaagggcgct	ctgtgagtca	gcctgctccc	ctccaggctt	gctcctcccc	caccagctc	3480
tcgtttccaa	tgcacgtaca	gcccgtacac	accgtgtgct	gggacacccc	ac	3532

<210> 91  
 <211> 204  
 <212> DNA  
 <213> HUMAN

<400> 91	
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caaacctgtg	agactttggc tccatctctg caaaagggcg ctctgtgagt cagcctgctc 120
ccctccaggc	ttgctcctcc cccaccagc tctcgtttcc aatgcacgta cagcccgtac 180
acaccgtgtg	ctgggacacc ccac 204

<210> 92  
 <211> 132  
 <212> DNA  
 <213> HUMAN

<400> 92	
ggatcctgtt	gactcgtgac cttacccccca accctgtgct ctctgaaaca tgagctgtgt 60
ccactcaggg	ttaaatggat taagggcggt gcaagatgtg ctttggttaa cagatgcttg 120
aaggcagcat	gc 132

<210> 93  
 <211> 275  
 <212> DNA  
 <213> HUMAN

<400> 93	
gcatagtgcc	aggtggtgcc ttgggttcca agctagtcca tggccccgat aaccttctgc 60
ctgtgcacac	acctgccccct cactccaccc ccctcctagc ttggtatgg gggagagggc 120
acagggccag	acaaacctgt gagactttgg ctccatctct gcaaaagggc gctctgtgag 180
tcagcctgct	ccccctccagg cttgctcctc ccccaccag ctctcgtttc caatgcacgt 240
acagcccgtg	cacaccgtgt gctgggacac cccac 275

<210> 94  
 <211> 89  
 <212> DNA  
 <213> HUMAN

<400> 94	
ctgctccccct	ccaggcttgc tcctccccca cccagctctc gtttccaatg cacgtacagc 60
ccgtacacac	cgtgtgctgg gacacccca 89

<210> 95  
<211> 61  
<212> DNA  
<213> HUMAN

<400> 95  
cacccagctc tcgtttccaa tgcacgtaca gcccgtagac accgtgtgct gggacacccc 60  
a 61

<210> 96  
<211> 116  
<212> DNA  
<213> HUMAN

<400> 96  
acctgcccct cactccaccc ccatacctagc tttggatatgg gggagagggc acagggccag 60  
acaaacctgt gagactttgg ctccatctct gcaaaagggc gctctgtgag tcagcc 116

<210> 97  
<211> 36  
<212> PRT  
<213> HUMAN

<400> 97  
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1 5 10 15  
Pro Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro Gly Glu  
20 25 30  
Glu Asp Leu Pro  
35

<210> 98  
<211> 6  
<212> PRT  
<213> HUMAN

<400> 98  
Gly Glu Glu Asp Leu Pro  
1 5

<210> 99  
<211> 4  
<212> PRT  
<213> HUMAN

<400> 99  
Glu Glu Asp Leu  
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<210> 100  
<211> 5  
<212> PRT  
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<400> 100  
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1 5

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<400> 101  
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1 5

<210> 102  
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<400> 102  
Glu Glu Asp Leu Pro Ser Glu  
1 5

<210> 103  
<211> 6  
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<400> 103  
Asp Leu Pro Gly Glu Glu  
1 5

<210> 104  
<211> 22  
<212> PRT  
<213> HUMAN

<400> 104  
Gly Gly Ser Ser Gly Glu Asp Asp Pro Leu Gly Glu Glu Asp Leu Pro  
1 5 10 15

Ser Glu Glu Asp Ser Pro  
20

<210> 105  
<211> 25  
<212> PRT

<213> HUMAN

<400> 105

Gly Glu Glu Asp Leu Pro Ser Glu Glu Asp Ser Pro Arg Glu Glu Asp  
1 5 10 15

Pro Pro Gly Glu Glu Asp Leu Pro Gly  
20 25

<210> 106

<211> 24

<212> PRT

<213> HUMAN

<400> 106

Glu Asp Pro Pro Gly Glu Glu Asp Leu Pro Gly Glu Glu Asp Leu Pro  
1 5 10 15

Gly Glu Glu Asp Leu Pro Glu Val  
20

<210> 107

<211> 7

<212> PRT

<213> HUMAN

<400> 107

Gly Glu Thr Arg Ala Pro Leu  
1 5

<210> 108

<211> 7

<212> PRT

<213> HUMAN

<400> 108

Gly Glu Thr Arg Glu Pro Leu  
1 5

<210> 109

<211> 7

<212> PRT

<213> HUMAN

<400> 109

Gly Gln Thr Arg Ser Pro Leu  
1 5

<210> 110

<211> 1247

<212> DNA

<213> HUMAN

<220>  
 <221> misc\_feature  
 <222> (1)..(1247)  
 <223> region 5' to the transcription initiation site as determined by RNase protection assay (nucleotide 3507 of SEQ ID NO: 5 and of Figures 2A-2F) in which an activating element is localized, which region corresponds to nucleotide 1328 to nucleotide 2574 of SEQ ID NO: 5 and of Figures 2A-2F.

<220>  
 <221> unsure what base is at position 647  
 <222> (647)  
 <223> unsure of the base at position 647, which is the same unknown base as that at position 1974 of SEQ ID NO: 5, and as that at position 1968 of SEQ ID NOS: 58 and 90. That unknown base at position 647 is in a region in which an activating element is localized and is 5' to the transcription initiation site.

<400> 110  
 tatgctactt tttgcagtc tttcattaca tttttctctc ttcatttgaa gagcatgtta 60  
 tatcttttag cttcacttgg cttaaaaggt tctctcatta gcctaacaca gtgtcattgt 120  
 tggtagcact tggatcataa gtggaaaaac agtcaagaaa ttgcacagta atacttggtt 180  
 gtaagaggga tgattcaggt gaatctgaca ctaagaaact cccctacctg aggtctgaga 240  
 ttcctctgac attgctgtat ataggctttt cctttgacag cctgtgactg cggactat 300  
 ttcttaagca agatatgcta aagttttgtg agcctttttc cagagagagg tctcatatct 360  
 gcatcaagtg agaacatata atgtctgcat gtttccatat ttcaggaatg tttgcttgtg 420  
 ttttatgctt ttatatagac agggaaactt gttcctcagt gacccaaaag aggtgggaat 480  
 tggtattgga tatcatcatt ggcccacgct ttctgacctt ggaaacaatt aagggttcat 540  
 aatctcaatt ctgtcagaat tggtagaaga aatagctgct atgtttcttg acattccact 600  
 tggtaggaaa taagaatgtg aaactcttca gttgggtgtg gtccctngtt tttttgcaat 660  
 ttccttctta ctgtgttaaa aaaaagtatg atcttgctct gagaggtgag gcattcttaa 720  
 tcatgatctt taaagatcaa taatataatc ctttcaagga ttatgtcttt attataataa 780  
 agataatttg tctttaacag aatcaataat ataatccctt aaaggattat atctttgctg 840  
 ggcgtagtgg ctcacacctg taatcccagc actttgggtg gccaaagggtg aaggatcaaa 900  
 tttgcctact tctatattat cttctaaagc agaattcatc tctcttccct caatatgatg 960  
 atattgacag ggtttgccct cactcactag attgtgagct cctgctcagg gcaggtagcg 1020  
 ttttttggtt ttgtttttgt ttttcttttt tgagacaggg tcttgctctg tcaccagggc 1080  
 cagagtgcaa tggtagagtc tcagctcact gcagcctcaa ccgcctcggc tcaaaccatc 1140  
 atcccatctt agcctcctga gtagctggga ctacaggcac atgccattac acctggctaa 1200  
 tttttttgta tttctagtag agacagggtt tggccatgtt gcccggg 1247

<210> 111  
 <211> 17  
 <212> DNA  
 <213> HUMAN

<400> 111  
 ctctgtgagt cagcctg 17

<210> 112  
 <211> 23  
 <212> DNA  
 <213> HUMAN

<400> 112

aggcttgctc ctccccacc cag 23

<210> 113  
<211> 18  
<212> DNA  
<213> HUMAN

<400> 113  
agactttggc tccatctc 18

<210> 114  
<211> 20  
<212> DNA  
<213> HUMAN

<400> 114  
cactccaccc ccatacctagc 20

<210> 115  
<211> 26  
<212> DNA  
<213> HUMAN

<400> 115  
gggagagggc acagggccag acaaac 26

<210> 116  
<211> 15  
<212> PRT  
<213> HUMAN

<400> 116  
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15